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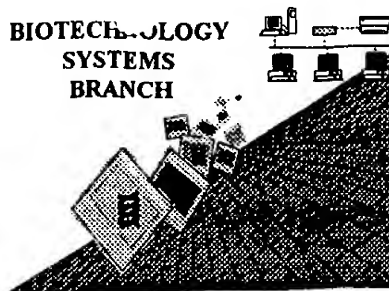
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M. Rao.

BIOTECHNOLOGY
SYSTEMS
BRANCH



#12
2/22/01

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/262,126B
Source: 1600 RUSH
Date Processed by STIC: 2/22/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1600

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

3 <110> APPLICANT: Miller, Brian S.
 4 Shetty, Jayarama K.
 6 <120> TITLE OF INVENTION: Modified Forms of Pullulanase
 9 <130> FILE REFERENCE: GC396-2
 11 <140> CURRENT APPLICATION NUMBER: 09/262,126B
 12 <141> CURRENT FILING DATE: 1999-03-03
 14 <160> NUMBER OF SEQ ID NOS: 9
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2794
 20 <212> TYPE: DNA
 21 <213> ORGANISM: B. deramificans
 23 <221> NAME/KEY: misc_feature
 24 <222> LOCATION: (1)...(2794)
 25 <223> OTHER INFORMATION: n = A, T, C, or G
 27 <400> SEQUENCE: 1

28	gatgggaaca	cgacaacgat	cattgtccac	tatttttggc	ctgctgggtga	ttatcaacct	60
29	tggagtctat	ggatgtggcc	aaaagacgga	ggtggggctg	aatacgattt	caatcaaccg	120
30	gctgactctt	ttggagctgt	tgcaagtgtc	gatattccag	gaaacccaag	tcaggtagga	180
31	attatcgctt	gcactcaaga	ttggaccaa	gatgtgagcg	ctgaccgcta	catagattta	240
32	agcaaaggaa	atgagggtgt	gctttagtaa	ggaaacagcc	aaatttttta	taatgaaaaa	300
33	gatgctgagg	atgcagctaa	acccgctgta	agcaacgctt	atttagatgc	ttcaaaccag	360
34	gtgctgggta	aacttagcca	gccgttaact	cttgggggaag	gnnnaagcgg	ctttacgggt	420
35	catgacgaca	cagcaaataa	ggatattcca	gtgacatctg	tgaaggatgc	aagtcttggt	480
36	caagatgtaa	cogctgtttt	ggcaggtacc	ttccaacata	tttttggagg	ttccgattgg	540
37	gcacctgata	atcacagtac	tttattaaaa	aagggtgacta	acaatctcta	tcaattctca	600
38	ggagatcttc	ctgaaggaaa	ctaccaatat	aaagtggctt	taaatgatag	ctggaataat	660
39	cogagttacc	catctgacaa	cattaattta	acagtccttg	ccggcgggtg	acacgtcact	720
40	ttttcgtata	ttccgtccac	tcattgcagtc	tatgacacaa	ttataaatcc	taatgaggat	780
41	ttacaagtag	aaagcggggt	taaaacggat	ctcgtgacgg	ttactctagg	ggaagatcca	840
42	gatgtgagcc	atactctgtc	cattcaaaca	gatggctatc	aggcaaagca	ggtgatacct	900
43	cgtaattgtc	tttaattcatc	acagtactac	tattcaggag	atgatcttgg	gaatacctat	960
44	acacagaaag	caacaacctt	taaagtctgg	gcaccaactt	ctactcaagt	aaatgttctt	1020
45	ctttatgaca	gtgcaacggy	ttctgtaaca	aaaatcgtac	ctatgacggc	atcgggccat	1080
46	ggtgtgtggg	aagcaacggt	taatcaaaac	cttgaaaatt	ggtattacat	gtatgaggta	1140
47	acaggccaag	gctctaccog	aacggctgtt	gatccttatg	caactgcgat	tgcaccaaat	1200
48	ggaacgagag	gcattgattgt	ggacctggct	aaaacagatc	ctgctggctg	gaacagtgat	1260
49	aaacatatta	gcgcaaaaga	tatagaagat	gaggtcatct	atgaaatgga	tgtccgtgac	1320
50	ttttccattg	accctaattc	gggtatgaaa	aataaaggga	agtatttggc	tcttacagaa	1380
51	aaaggaacaa	agggccctga	caacgtaaag	acggggatag	attccttaaa	acaacttggg	1440
52	attactcatg	ttcagcttat	gcctgttttc	gcatctaaca	gtgtcgatga	aactgatcca	1500
53	accaagata	attggggtta	tgacctcgc	aactatgatg	ttcctgaagg	gcagtatgct	1560
54	acaaatgcga	atggtaatgc	tcgtataaaa	gagtttaagg	aaatggttct	ttcactccat	1620
55	cgtgaacaca	ttggggttat	catggatggt	gtctataatc	atacctttgc	cacgcaaatc	1680
56	tctgacttcg	ataaaaattgt	accagaatat	tattaccgta	cgatgatcca	ggtaattata	1740
57	ccaacggatc	aggtactgga	aatgaaattg	cangcngaaa	ggccaatggt	tcaaaaattt	1800
58	attattgatt	cccttaagta	ttgggtcaat	gagtatcata	ttgacggctt	ccgttttgac	1860

pp 1-2, 5
 Does Not Comply
 Corrected Diskette Needed

same error as
previous submission

→ <2207> insert this MANDATORY
 name identifier

whenever

<2217>, <2227>,
 or <2237> is
 shown.

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

59 ttaatggcgc tgcttggaag agacacgatg tccaaagctg cctcggagct tcatgctatt 1920
 60 aatccaggaa ttgcacttta cggtagagcca tggacgggtg gaacctctgc actgccagat 1980
 61 gatcagcttc tgacaaaagg agctcaaaaa ggcattggag tagcgggtgt taatgacaat 2040
 62 ttacgaaacg cgttggaacg caatgtcttt gattcttccg ctcaagggtt tgcgacaggt 2100
 63 gcaacagget taactgatgc aattaagaat ggcgttgagg ggagtattaa tgactttacc 2160
 64 tcttcaccag gtgagacaat taactatgtc acaagtcacg ataactacac cctttgggac 2220
 65 aaaatagccc taagcaatcc taatgattcc gaagcggatc ggattaaaat ggatgaactc 2280
 66 gcacaagcag ttgttatgac ctacacaagg gttccattca tgcaaggcgg ggaagaaatg 2340
 67 cttegtanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcggg caatgagttt 2400
 68 gattggagca ggaagctca atattccagat gttttcaact attatagcgg gctaattcac 2460
 69 ctctgtcttg atcaccacgc cttccgcatg acgacagcta atgaaatcaa tagccacctc 2520
 70 caattcctaa atagtccaga gaacacagtg gcctatgaat taactgatca tgttaataaa 2580
 71 gacaaatggg gaaatatcat tgttgtttat aacccaaata aaactgtagc aaccatcaat 2640
 72 ttgccgagcg gyaatgggc aatcaatgct acgagcggta aggtaggaga atccaccctt 2700
 73 ggtcaagcag aggggaagtgt ccaagtacca ggtatatcta tgatgatcct tcatcaagag 2760
 74 gtaagccag accacggtaa aaagtaatag aaaa 2794

76 <210> SEQ ID NO: 2

77 <211> LENGTH: 958

78 <212> TYPE: PR1

79 <213> ORGANISM: B. deramificans

81 <220> FEATURE:

82 <221> NAME/KEY: VARIANT

83 <222> LOCATION: (1)...(956)

84 <223> OTHER INFORMATION: Xaa = Any Amino Acid

86 <220> FEATURE:

87 <221> NAME/KEY: VARIANT

88 <222> LOCATION: (957)...(957)

89 <223> OTHER INFORMATION: Xaa = gap of indeterminate length

91 <400> SEQUENCE: 2

92 Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
 93 1 5 10 15
 94 Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
 95 20 25 30
 96 Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
 97 35 40 45
 98 Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr
 99 50 55 60
 100 Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
 101 65 70 75 80
 102 Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
 103 85 90 95
 104 Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
 105 100 105 110
 106 Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
 107 115 120 125
 108 Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
 109 130 135 140
 110 Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
 111 145 150 155 160

Xaa can only represent
a single amino acid.

Per 1.822(d)(5)(e) of
new sequence rules,

"A sequence with a
gap or gaps shall
be presented as a
plurality of
separate sequences..."

However, since only
one amino acid
follows gap, and
at least four
amino acids are
needed for a sequence,
delete last amino
acid and adjust
2117 response to 957

see p. 5

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

```

W--> 112 Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
      113          165          170          175
      114 Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val
      115          180          185          190
      116 Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
      117          195          200          205
      118 Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Lys Val Thr Asn Asn
      119          210          215          220
      120 Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr Lys
      121          225          230          235          240
      122 Val Ala Leu Asn Asp Ser Trp Asn Asn Ser Tyr Pro Ser Asp Asn Ile
      123          245          250          255
      124 Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile
      125          260          265          270
      126 Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro Asn Ala Asp
      127          275          280          285
      128 Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu
      129          290          295          300
      130 Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly
      131          305          310          315          320
      132 Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu Asn Ser Ser Gln
      133          325          330          335
      134 Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala
      135          340          345          350
      136 Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu
      137          355          360          365
      138 Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile Val Pro Met Thr
      139          370          375          380
      140 Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu
      141          385          390          395          400
      142 Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr
      143          405          410          415
      144 Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn Gly Thr Arg Gly
      145          420          425          430
      146 Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp
      147          435          440          445
      148 Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met
      149          450          455          460
      150 Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly Met Lys Asn Lys
      151          465          470          475          480
      152 Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp Asn
      153          485          490          495
      154 Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly Ile Thr His Val
      155          500          505          510
      156 Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp Glu Thr Asp Pro
      157          515          520          525
      158 Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp Val Pro Glu
      159          530          535          540
      160 Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe

```

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

```

161 545          550          555          560
162 Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile Gly Val Asn Met
163          565          570          575
164 Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile Ser Asp Phe Asp
165          580          585          590
166 Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile
167          595          600          605
W--> 168 Pro Thr Asp Gln Val Leu Glu Met Lys Leu Xaa Ala Glu Arg Pro Met
169          610          615          620
170 Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp Val Asn Glu Tyr
171          625          630          635          640
172 His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp
173          645          650          655
174 Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile
175          660          665          670
176 Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
177          675          680          685
178 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
179          690          695          700
180 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
181          705          710          715          720
182 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
183          725          730          735
184 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
185          740          745          750
186 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
187          755          760          765
188 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
189          770          775          780
190 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
191          785          790          795          800
W--> 192 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
193          805          810          815
194 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
195          820          825          830
196 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
197          835          840          845
198 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
199          850          855          860
200 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
201          865          870          875          880
202 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
203          885          890          895
204 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
205          900          905          910
206 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
207          915          920          925
208 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
209          930          935          940

```

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

W--> 210 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys Xaa *Lys delete*
 211 945 950 955
 213 <210> SEQ ID NO: 3
 214 <211> LENGTH: 718
 215 <212> TYPE: PRT
 216 <213> ORGANISM: B. subtilis
 218 <400> SEQUENCE: 3
 219 Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
 220 1 5 10 15
 221 Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
 222 20 25 30
 223 Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
 224 35 40 45
 225 Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
 226 50 55 60
 227 His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
 228 65 70 75 80
 229 His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
 230 85 90 95
 231 Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
 232 100 105 110
 233 Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
 234 115 120 125
 235 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
 236 130 135 140
 237 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
 238 145 150 155 160
 239 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
 240 165 170 175
 241 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
 242 180 185 190
 243 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
 244 195 200 205
 245 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
 246 210 215 220
 247 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
 248 225 230 235 240
 249 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
 250 245 250 255
 251 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
 252 260 265 270
 253 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
 254 275 280 285
 255 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
 256 290 295 300
 257 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
 258 305 310 315 320
 259 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
 260 325 330 335

VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:02

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2